FORM PTO-1449

INFORMATION DISCLOSURE CITATION

Atty Docket 24460	Serial No. 09/718,425
Applicant BECKER, TOPF	
Filing Date Nov. 24, 2000	Group Art Unit 1645

U.S. PATENT DOCUMENTS

Examiner Initial		Document Number	Issue Date	Name	Class	Sub-Class	Filing Date
	AA						

FOREIGN PATENT DOCUMENTS

		Document Number	Date	Country	Class	Sub-Class	Trans-lation
	AB						

OTHER (Including Author, Title, Date, Pertinent Pages, etc.)

	AC		Bahar, I., et al., "Short-Range Conformational Energies, Secondary Structure Propensities, and Recognition of Correct Sequence-Structure Matches". PROTEINS: Structure, Function, and Genetics, 29:292-308 (1997).
	AD		Beauregard, M., et al., "Spectroscopic investigation of structure in octarellin (a *de novo* protein designed to adopt the α/β-barrel packing". Protein Engineering, 4:745-749 (1991).
	AE		Betz, Stephen F., et al., "Native-like and structurally characterized designed α-helical bundles". Current Opinion in Structural Biology, 5:457-463 (1995).
	AF		Bernstein, Frances C., et al., "The Protein Data Bank: A Computer-based Archival File for Macromolecular Structures". J. Mol. Biol., 112:535-542 (1977).
	AG		Betz, Stephen F., et al., "Controlling Topology and Native-like Behavior of *de Novo*-Designed Peptides: Design and Characterization of Antiparallel Four-Stranded Coiled Coils". Biochemistry, 35:6955-6962 (1996).
	AH		Brooks, Bernard R., et al., "CHARMM: A Program for Macromolecular Energy, Minimization, and Dynamics Calculations". Journal of Computational Chemistry, 4:187-217 (1983).
	AI		Connolly, Michael L., "Solvent-Accessible Surfaces of Proteins and Nucleic Acids". Science, 221: 709-713 (1983).
	AJ		Dahiyat, Bassil I., et al., "Protein design automation". Protein Science, 5:895-903 (1996).
	AK		Dahiyat, Bassil I., et al., "Probing the role of packing specificity in protein design". Proc. Natl. Acad. Sci. USA, 94:10172-10177 (1997).
	AL		Desjarlais, John R., et al., "De novo design of the hydrophobic cores of proteins". Protein Science, 4:2006-2018 (1995).
	AM		Desmet, Johan, et al., "The dead-end elimination theorem and its use in protein side-chain positioning". Nature 356:539-542 (1992).

Examiner	Date Considered 7/20/02

EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP § 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to Applicant.

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	BA						

FOREIGN PATENT DOCUMENTS

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	BB						

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	BC		Fezoui, Youcef, et al., "*De novo* design and structural characterization of an α-helical hairpin peptide: A model system for the study of protein folding intermediates". Proc. Natl. Acad. Sci. USA, 91:3675-3679 (1994).
	BD		Harbury Pehr R., et al., "Repacking protein cores with backbone freedom: Structure prediction for coiled coils". Proc. Natl. Acad. Sci. USA, 92:8408-8412 (1995).
	BE		Hecht, Michael H., et al., "De Novo Design, Expression, and Characterization of Felix: A Four-Helix Bundle Protein of Native-Like Sequence". Science, 249:884-891 (1990).
	BF		Hellinga, Homme W., et al., "Constructions of New Ligand Binding Sites in Proteins of Known Structure". J. Mol. Biol., 222:763-785 (1991).
	BG		Herzyk, Pawel, et al., "A Reduced Representation of Proteins for Use in Restraint Satisfaction Calculations". PROTEINS: Structure, Function, and Genetics, 17:310-324 (1993).
	BH		Hurley, James H., et al., "Design and Structural Analysis of Alternative Hydrophobic Core Packing Arrangements in Bacteriophage T4 Lysozyme". J. Mol. Biol., 224:1143-1159 (1992).
	BI		Jones, David T., "De novo protein design using pairwise potentials and a genetic algorithm". Protein Science, 3:567-574 (1994).
	BJ		Jorgensen, William L., et al., "Comparison of simple potential functions for simulating liquid water". J. Chem. Phys., 79:926-935 (1983).
	BK		Kamtekar, Satwik, et al., "Protein Design by Binary Patterning of Polar and Nonpolar Amino Acids". Science, 262:1680-1685 (1993).
	BL		Klemba, Michael, et al., "Novel metal-binding proteins by design". Structural Biology, 2:368-373 (1995).
	BM		Kono, Hidetoshi, et al., "Energy Minimization Method Using Automata Network for Sequence and Side-Chain Conformation prediction From Given Backbone Geometry". PROTEINS: Structure, Functions, and Genetics, 19:244-255 (1994).

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	CA						

FOREIGN PATENT DOCUMENTS

		Document Number	Date	Country	Class	Sub-Class	Trans-lation
	CB						

OTHER (Including Author, Title, Date, Pertinent Pages, etc.)

	CC		Kortemme, Tanja, et al., "Design of a 20-Amino Acid, Three-Stranded β-Sheet Protein". Science, 281:253-256 (1998).
	CD		Kuroda, Yutaka, et al., "Solution Structure of a *de Novo* Helical Protein by 2D-NMR Spectroscopy". J. Mol. Biol., 236: 862-868 (1994).
	CE		Lau, Kit Fun, et al., "Theory for protein mutability and biogenesis". Proc. Natl. Acad. Sci. USA, 87:638-642 (1990).
	CF		Lazar, Greg A., et al., "De novo design of the hydrophobic core of ubiquitin". Protein Science, 6:1167-1178 (1997).
	CG		MacKerell, A. D., Jr., et al., "All-Atom Empirical potential for Molecular Modeling and Dynamics Studies of Proteins". J. Phys. Chem. B, 102:2586-3616 (1998).
	CH		Malakauskas, Sandra M., et al., "Design, structure and stability of a hyperthermophilic protein variant". Nature Structural Biology, 5:470-475 (1998).
	CI		Metropolis, Nicholas, et al., "The Monte Carlo Method". Journal of the American Statistical Association, 247:335-341 (1949).
	CJ		Miyazawa, Sanzo, et al., "Residue-Residue Potentials with a Favorable Contact Pair Term and an Unfavorable High Packing Density Term, for Simulation and Threading". J. Mol. Biol., 256:623-644 (1996).
	CK		Nautiyal, Shivani, et al., "A Designed Heterotrimeric Coiled Coil". Biochemistry, 34:11645-11651 (1995).
	CL		Pveletich, Nikola P., et al., "Zinc Finger-DNA Recognition: Crystal Structure of a Zif268-DNA Complex at 2.1 Å". Science, 252:809-817 (1991).
	CM		Ponder, Jay W., et al., "Use of Packing Criteria in the Enumeration of Allowed Sequences for Different Structural Classes". J. Mol. Biol., 193:775-791 (1987).

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	DA						

FOREIGN PATENT DOCUMENTS

		Document Number	Date	Country	Class	Sub-Class	Trans-lation
	DB						

OTHER (Including Author, Title, Date, Pertinent Pages, etc.)

	DC		Quinn, Thomas P., et al., Betadoublet: *De novo* design, synthesis, and characterization of a β-sandwich protein". Proc. Natl. Acad. Sci. USA, 91:8747-8751 (1994).
	DD		Raleigh, Daniel P., et al., "A *de Novo* designed Protein Mimics the Native State of Natural Proteins". J. Am. Chem. Soc., 117:7558-7559 (1995).
	DE		Regan, Lynne, et al., "Characterization of a Helical protein designed from First Principles". Science, 247:976-978 (1988).
	DF		Rost, Burkhard, et al., "Prediction of protein Secondary Structure at Better than 70% Accuracy". J. Mol. Biol., 232:584-599 (1993).
	DG		Salamov, Asaf A., et al., "Prediction of Protein Secondary Structure by Combining Nearest-neighbor Algorithms and Multiple Sequence Alignments" J. Mol. Biol., 247:11-15 (1995).
	DH		van Gunsteren, W. F., et al., "Algorithms for macromolecular dynamics and constraint dynamics". Molecular Physics, 34:1311-1327 (1977).
	DI		
	DJ		
	DK		
	DL		
	DM		

Examiner	Date Considered 9/20/05

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